

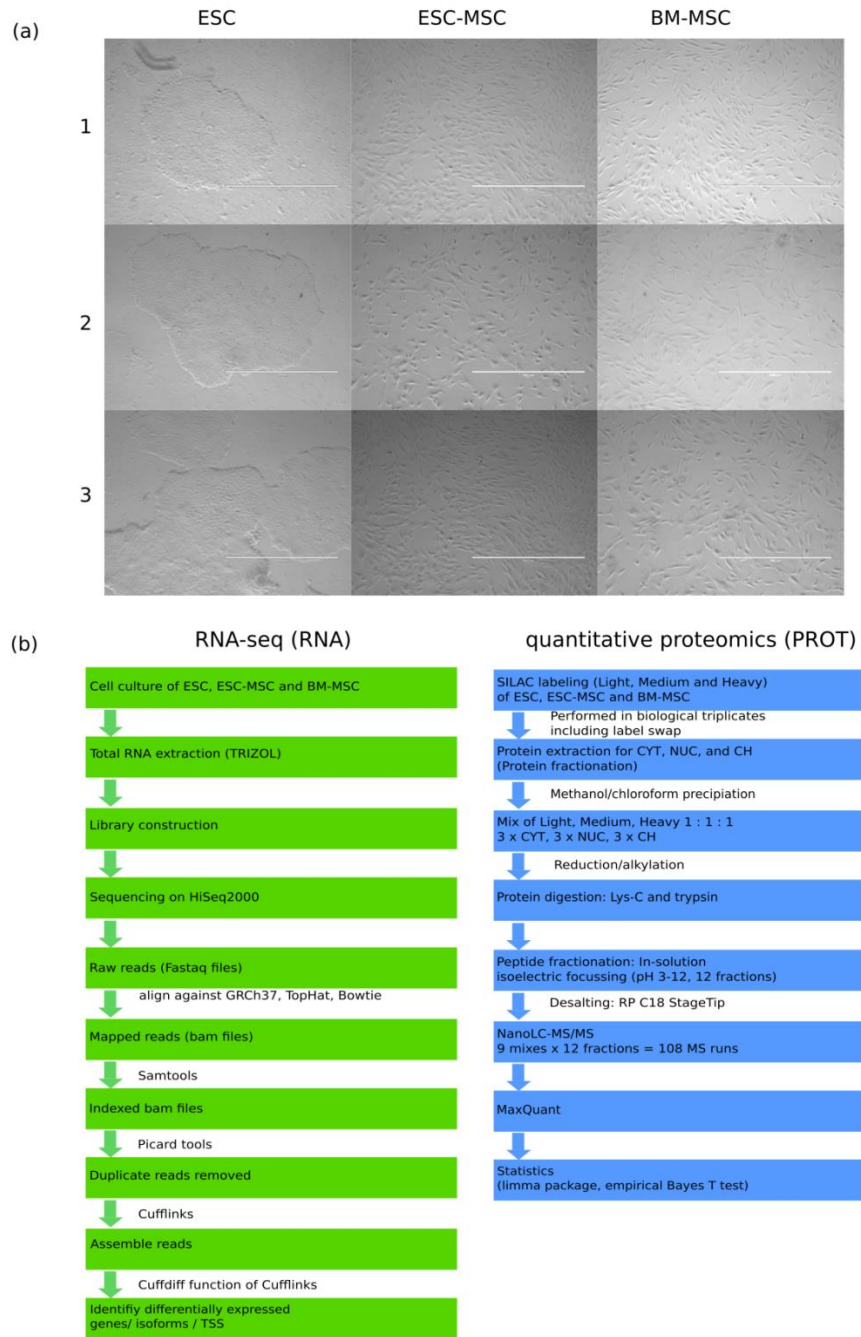
Supplementary Information

Comprehensive transcriptomic and proteomic characterization of human mesenchymal stem cells reveals source specific cellular markers

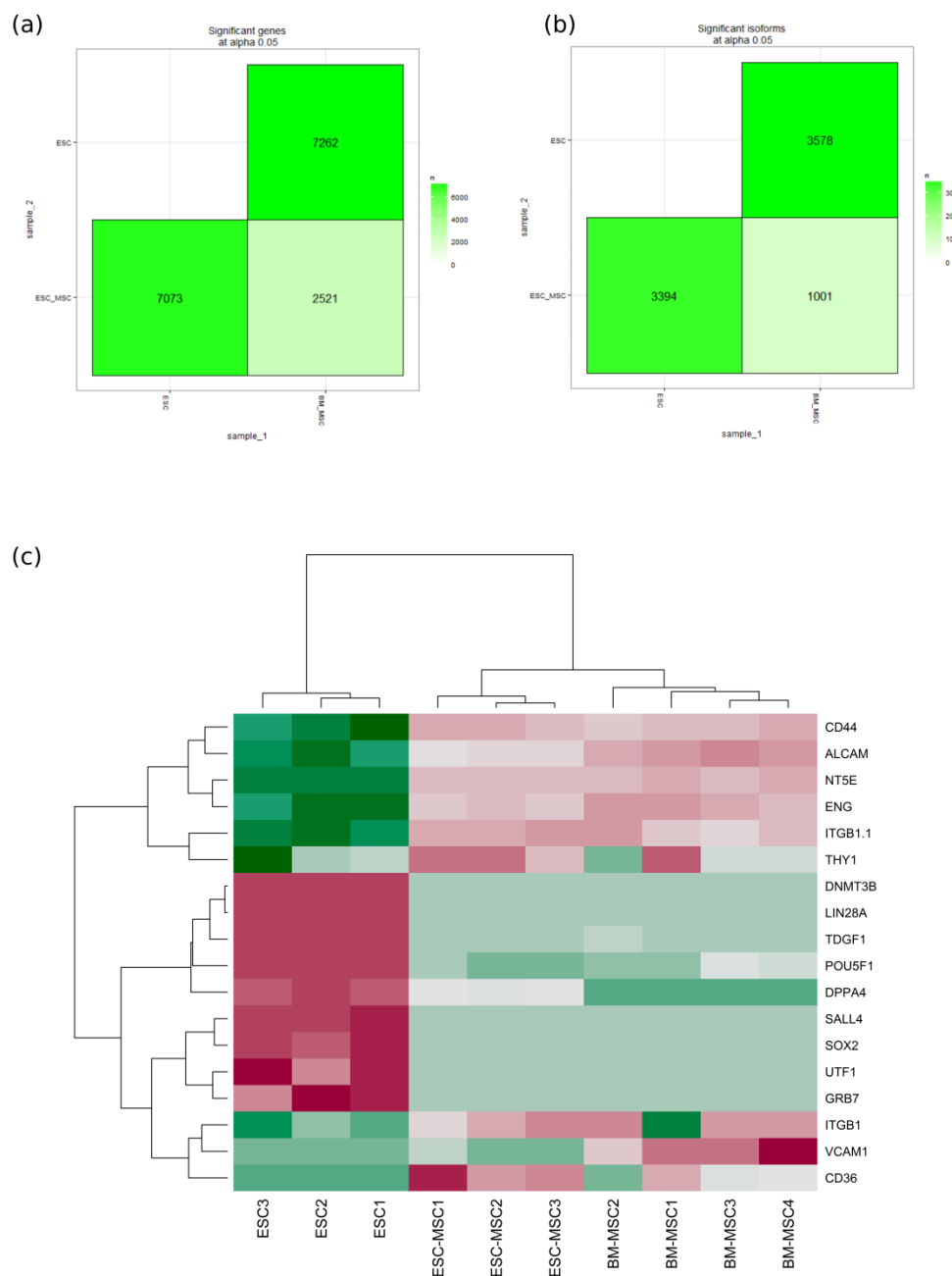
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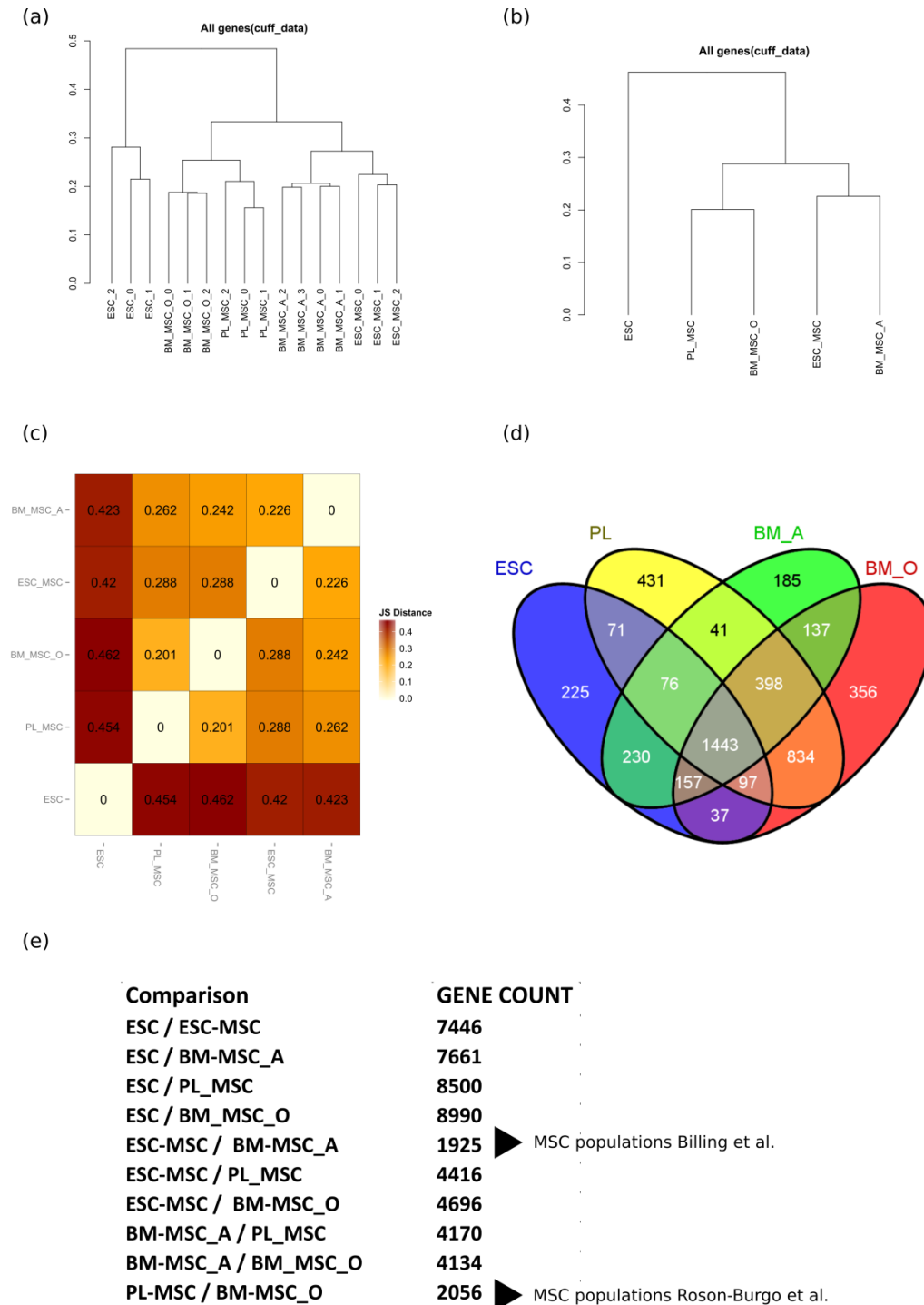
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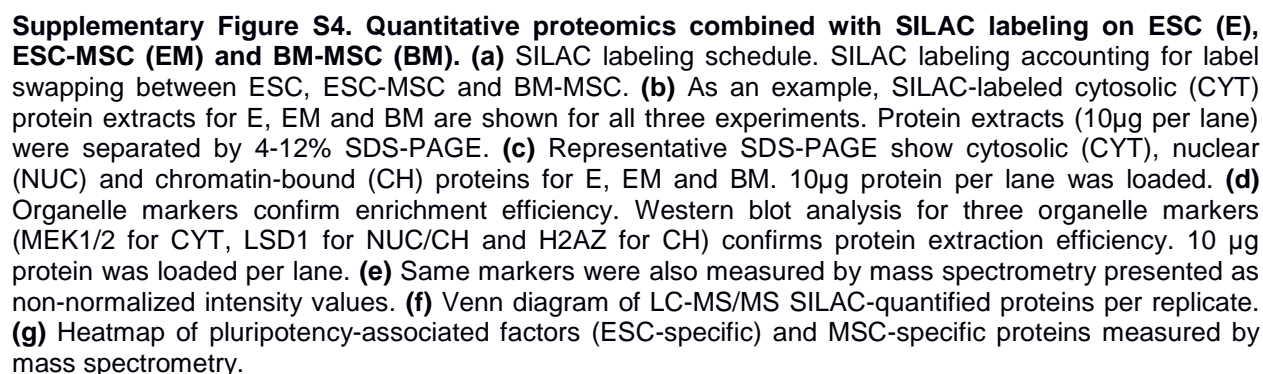
Supplementary Figure S1. ESC-derived MSC (ESC-MSC) were compared to their origin ESC as well as to bone marrow-derived MSC (BM-MSC) with two high throughput techniques: RNA deep sequencing (RNA) and LC-MS/MS (PROT). (a) Representative microscope images of ESC, ESC-MSC and BM-MSC for the three experiments. ESC-MSC in the study were derived from three independent differentiation experiments. BM-MSC were derived from four donors, with three of them used in proteomics. Details of the BM-MSC used; 40y/m (StemCell, MSC-001F, lot#BM2893), 39/m (Lonza, PT2505, lot#1F3422), 27y/m (Lonza, PT2505, lot#318006), 20y/m (only in RNA-seq, Lonza, PT2505, lot#8F3520). **(b)** Pipelines of RNA and PROT.

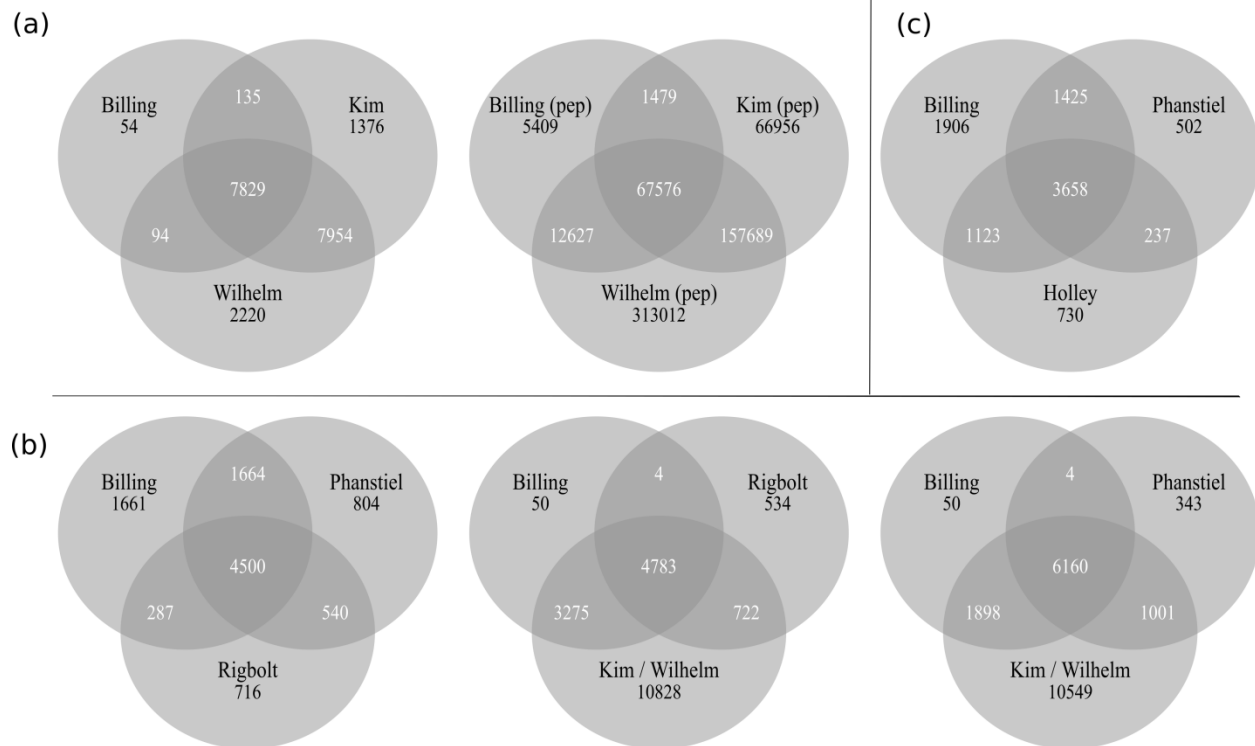


Supplementary Figure S2. Significant differentially expressed (a) genes and (b) isoforms (FDR < 0.05) based on RNA-seq for the following comparisons: ESC-MSC vs ESC, BM-MSC vs ESC and BM-MSC vs ESC-MSC. Plots were derived with the CummeRbund package. (c) Heatmap of ESC- and MSC-specific marker genes.



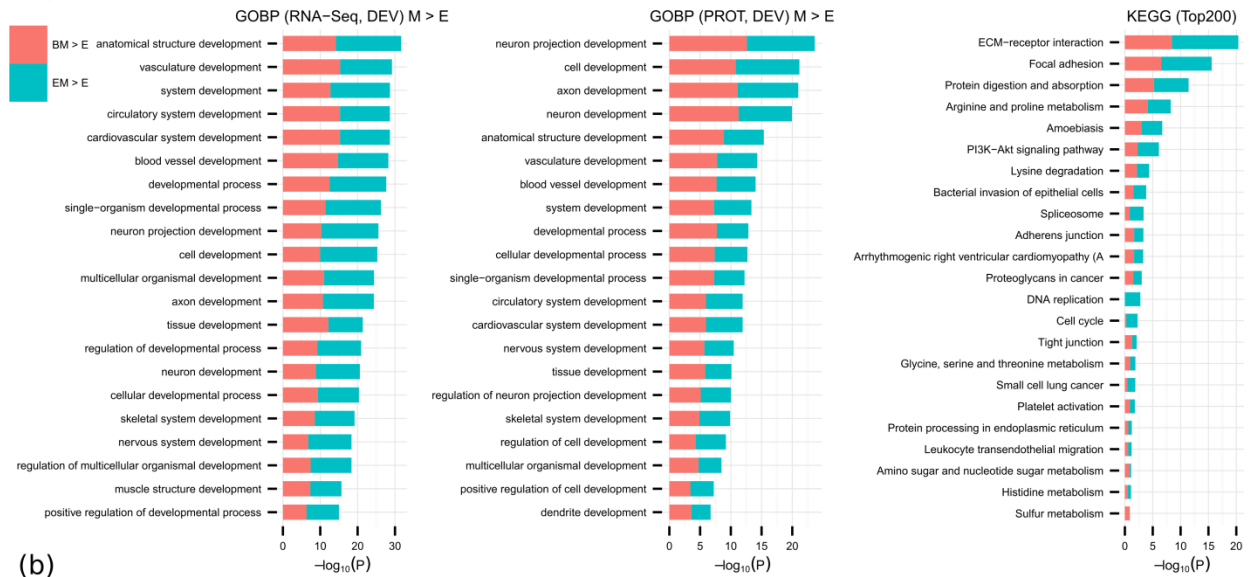
Supplementary Figure S3. Comparison of RNA-seq data with other MSC study¹. Both data sets were analyzed by the same bioinformatics pipeline (see materials and methods section). Dendrograms on (a) replicates and (b) groups show clear separation of ESC from MSC (placenta-derived MSC (PL_MSC), bone marrow-derived MSC (BM_MSC), ESC-derived MSC (ESC_MSC)). In both studies, fetal and adult MSC were compared. In our study: ESC-MSC vs BM-MSC (_A), by Roson-Burgo et al.: PL-MSC vs BM-MSC (_O). (c) Distance matrix generated by CummeRbund. (d) Venn diagram of up-regulated proteins (FDR < 0.05) in different MSC populations when compared to ESC. (e) Gene counts of all pairwise comparisons (FDR < 0.05).



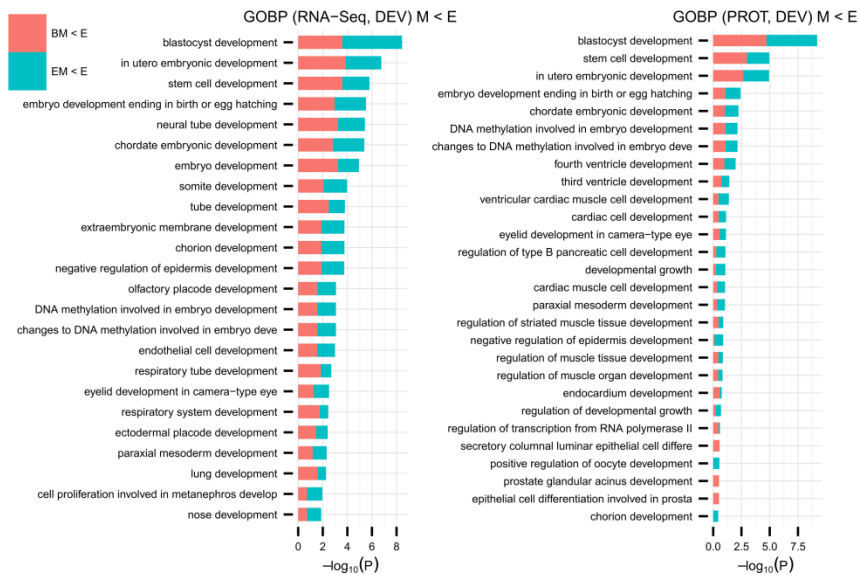


Supplementary Figure S5. Comparing presented proteomics data set with other studies. (a) Comparison with the human proteome maps^{2,3} at protein and peptide level. **(b)** Comparison with the largest proteomics data sets available for ESC^{4,5} at protein level. **(c)** Comparison with the largest proteomics data set available for MSC⁶.

(a)



(b)



Supplementary Figure S6. Enrichment analysis for GOBP terms filtered for "development". Comparing MSC vs ESC with genes/proteins (a) up-regulated in MSC and (b) up-regulated in ESC. Enrichment was performed on RNA-seq (left panels) and proteomics data (right panels) using the comics package. Bar charts represent the most significant top 20 terms for each cell type sorted by the mean of $-\log_{10} p$ values.

Supplementary Table S3

The enrichment files can be downloaded using the following link:

<https://bitbucket.org/billingetal2015c/disseminatebilling2015/downloads>

REFERENCES

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4. Phanstiel, D. H. *et al.* Proteomic and phosphoproteomic comparison of human ES and iPS cells. *Nat. Methods* **8**, 821–827 (2011).
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6. Holley, R. J. *et al.* Comparative Quantification of the Surfaceome of Human Multipotent Mesenchymal Progenitor Cells. *Stem Cell Rep.* **4**, 473–488 (2015).